

Alignment of head 9
against sequence
of chromosome 19

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2002, 15:05:56 ; Search time 12.61 Seconds
(without alignments)
4.558 Million cell updates

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Title:
Perfect score: 824
Sequence: 1 cagctcgaacgaac

```

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.0

Searched: 2 seqs, 34875 residues

Total number of hits satisfying chosen parameters: 4

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : ac005329.seq:★

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	88.2	32760	1 AC005329_1	Sequence ac005329
2	94.8004	11.5	32760	1 AC005329_1	Sequence ac005329

ALIGNMENTS

```

RESULT 1
AC005329.1
; Sequence ac005329: residues 1 to 32760
; TOIG of: ac005329 check: 3646 from: 1 to: 34875
;
; LOCUS AC005329 34875 bp DNA PRI 28-JUL-1998
; DEFINITION Homo sapiens chromosome 19, cosmid R34382, complete sequence.
; ACCESSION AC005329
; VERSION AC005329.1 GI:3342732
; KEYWORDS HTG.
; SOURCE human.
; ORGANISM Homo sapiens

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Query Match 88.2%; Score 727; DB 1; Length 32760;
Best Local Similarity 4.1%; Pred. No. 0;
Matches 813; Conservative 0; Mismatches 10; Indels 18942; Gaps 8;

Qy	1	cgggctcgagcgctcgagcgggaaacgggagcgctaaaggagaacgacccacagagttgt	60
Db	7458	CGCTTTGGCGCGGCCCGCGGAACCGGAGCGCTAAGGAAACGGACCTCAGAGTTGT	7517
Qy	61	ctgaagggccgagggccaagtggcggtgctgt-----	91
Db	7518	CTGAAGGCCGAGGCCCAACATGGCGGTGCTGTCAAGTGAGCGGCACCGCGCGCGGTGT	7577
Qy	92	Position 1-14	91

CDNA of thylakoid et al.
Figure 1

[illegible]

Db 8658 CAAGCAATCTCCACCTGAGCCTCCAAAGTCTGGGAGCCACGGCACCCACCTACGC 8717
QY 92 ----- 91
Db 8718 TAAGATTGAATGAGGGCTAAATTTCCATAAGATGCTGTGACACAAAGACATATA 8777
QY 92 ----- 91
Db 8778 TTTTATTTCCAAAGCAAAATTCAGATTCTGTAATCCTCACCAGGCCCTTGTGTAAGATG 8837
QY 92 ----- 91
Db 8838 CCTGGCCACGCGGGTGGCTCAGGCTGTAAATCCAGCACTTTGGAAGCCCAAGGTGG 8897
QY 92 ----- 91
Db 8898 CGGATCACCTGAGTCCGGAGTTGAGACACCGCTGSCCAACATGGAGAAACCCGCTC 8957
QY 92 ----- 91
Db 8958 TACTAAAAATACAAAATCAGTGGTGTGGTGGCGCATGCTGTAATFCGAGTACTGGG 9017
QY 92 ----- 91
Db 9018 GGGCTGGGGCAAGAAATCGGTTGAACCCGGGAGCGGAGGTTGCAGTGAGCTAAGATTG 9077
QY 92 ----- 91
Db 9078 CACCATTCACCTCCATCCTGGGCAACAAGAGTGAACCTCTCAAAAAACAAAAACAAA 9137
QY 92 ----- 91
Db 9138 AACAAACAGCTGGGCGTGGTGGCTCAGGCTGTAAATCCAGCACTTTGGGAGGCCGAGG 9197
QY 92 ----- 91
Db 9198 TGGCGGATCCCTGAGTTCGGGAGTTCAAGACCAGCCTGATCAACATGGAGAAACCCG 9257
QY 92 ----- 91
Db 9258 TCTCTACTAAAAATGCAAAATTAGCTGAGGTTGGTAGAGGCCCTGTATCCAGCTA 9317
QY 92 ----- 91
Db 9318 CTCGGAGGCTGAGGAGGAGATAGCTTGAACCTGGGAGGTGAGGTTGCAGTGAGCCA 9377
QY 92 ----- 91
Db 9378 AGATTGTCCGTTGCACCTCCAGCCTGGGTGACAAAGAGGAAACTCCGCTCTCAAAACA 9437
QY 92 ----- 91
Db 9438 ACAACAACAACAAACCTGACCCAGAGGACAGAAATCCCATCAGCTCAGAGTTCTCA 9497
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QY 92 ----- 91
Db 9618 GTGCCAGCCTCAGGCATGCCAAGAAGTAGTCAAGGCTTTGTCTTTCAGAGATTGT 9677
QY 92 ----- 91
Db 9678 GGCCTGGAGGGCCATGGGAAACAGCAACCCGGATGAGCTAAGGCTGGGGTGAGGA 9737
QY 92 ----- 91
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QY 92 ----- 91
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QY 92 ----- 91
Db 9858 AAGTACCATCACCTGGGAGCTTCAACAGAGCTGATTGTTCTCACAGATTCTGGGGCT 9917
QY 92 ----- 91
Db 9918 GGAAGCCAAAGATTGGGGTCAGCAGGTTGGTTCTCTGCTGAGGCTCTGCTTGGCTT 9977
QY 92 ----- 91
Db 9978 GCGCTGGCCATCTTCTCCCTCGCTTTCTCTCTACATGTTTGTGCTGATCGCCTT 10037
QY 92 ----- 91
Db 10038 TTCTTACAGGACATAAGTCATATCGGATGAGGGCCACCTCGTGACCTCACTGCTCTT 10097
QY 92 ----- 91
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QY 92 ----- 91
Db 10518 ACCAAGCTGCCTTTCTGGATTCTTCTGTGAGCCAGGATCTCTGGCCTTCCAGGTTT 10577
QY 92 ----- 91
Db 10578 CCTCCGCTGAGTGCCTCGGCGGTGGCAAGGCCCTCTCTGCTTGTAGTCTTTCGCTCG 10637
QY 92 ----- 91
Db 10638 GAAGGCTCTCCAGGAGACTTCGTGAGCGGCGTTCCCTCTCTGCGCTTCTTTGAGGC 10697
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Db 10698 TGCTCTCTAGGGTGTCTTCTGTGTAGATTGACGTGGGAGCGCCCTCCCGCTTAG 10757
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QY 92 ----- 91
Db 10818 GCAGCCAGGCGCTGGAGACCCACGCTTGTGAGGCACAGCTGTCAGGCCAGGAGGAG 10877

QY	306	-----	305
Db	14178	GAGAGTGGCTGGAGCCCCCTGTGGAATGTTGGGACTTAGGATACACTGGGTTCCAGGAA	14237
QY	306	-----	305
Db	14238	CTATGTGATGAGGACAGATCTACCCGTTTCTCTATTTATGTAATTGTAATGTGGCTG	14297
QY	306	-----	305
Db	14298	GTGGGCGCGCTTTACAACTCTTGGGGCCGAGGCCACCTGCAGGAGCGGCTGTGCCTC	14357
QY	306	-----	305
Db	14358	TCACCTCTGCCGGCTGCCGCCCGGACATGAGTCGGGGGTTCTGGGTGCTCCACGTGA	14417
QY	306	-----	305
Db	14418	GTCTCAGCTTGGGCCACCGCGGGCTCCGGGGGTGGGCTCTCACCCGAGCCGCCCTCCGC	14477
QY	306	-----	364
Db	14478	AGATTCCTGTGGCCCATGACCTTCGGCCTGGCTGTGGCCCTGGAGATGATGCA	14537
QY	365	tgccagcaccgcgtacgacatggacgctttggcggtcttcgcgcgcagccgcgcgc	424
Db	14538	TGGCAGCACCCCGCTACGACATGGACCGCTTTGGCGTGGTCTCCGGGCCAGCCGCGCC	14597
QY	425	agtcgagctcatgactgtgcccggcacactcaccacaaagatggccccagcgttcgca	484
Db	14598	AGTCGACGTCATGATCGTGGCCGGCACACTCACCAAGAATGGCCCGGCTTCGCA	14657
QY	485	-----	484
Db	14658	AGGTAGGCGCTGTCCCGAGCCGCCAGCGCCGCCACAGGTGAGCTGGCAGCAGCCCCGCC	14717
QY	485	-----	531
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QY	532	-----	531
Db	14778	AGTGCAGGCGGGGGTCTCCAGGACAGAGTAGCGTGAAGTGGCTGGCGCTGCCG	14837
QY	532	-----	531
Db	14838	TGATGGCGCTTATCAAAAGTGTCTATCATTCAGTGAATCCACGTGGTCCCGCGCT	14897
QY	532	-----	531
Db	14898	GCCCTTCAGCCGCTCTCGGTGCTCACCCTAGGCAGATGCGCTGGTGGGCTCTCCCCAG	14957
QY	532	-----	531
Db	14958	AACGATTCTCCATCCACCCACGACAGCAGACCCACATTCGCCAGTTCCTGTGCTT	15017
QY	532	-----	531
Db	15018	TACTCACACATAAGTGATGACAGGTGCTAGATAGTTTTATATCTCAGCCTTCTCACT	15077
QY	532	-----	531
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Db	15138	CAGGCTGGAGTGGGTGGAACCATCTCGGCTCACTGCAACCTCCGCCCTCCAGGTTCAAG	15197
QY	532	-----	531
Db	15198	CAATTTTCCCTCACCCCTCCCAAGTAGCTGGGATTCACAGCATGCACCCACACCCA	15257

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Db 19698 GGCTTTGGGGAACCTGACTCCACCCACCAGCCCTTCATCCGTCGAAGTCCAGGCCT 19757
QY 810 ----- 809
Db 19758 CATCAGGAGCGTCATTCATTACAGAAAGCTCCCATCTTCTGTGTTCAGCGCCAGATCC 19817
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Db 19818 CGCCGCTGTGGACCTCGCTCTGACAGGCCACCCCTGCATGCTGTCACACAGGAGC 19877
QY 810 ----- 809
Db 19878 AGTTCTGGGGATCGGCAGTTATGACGGGCCAGGCTGGGATGGGGCCCGGAGACTGGGCG 19937
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Db 20298 AAATGGGAGCTTGGGAACGGGCTGTACAGAGCCACGCCCTCTGGGGCGGAGGAG 20357
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Tue Mar 5 15:12:34 2002

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Db 21978 ATCACAGGTGTAGCCACACGCGCCAGCTGANTTCCATTTTTTTTTTAAATTTTCTTTC 22037
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QY 810 ----- 809
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Qy 810 ----- 809

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Qy 810 ----- 809
Db 26118 CTGGGTGGGTCTGTGCTGTATAGCCGTTTCTTCCCTCTGAGCGTGGGGCCACA 26177
Qy 810 ----- 809

Tue Mar 5 15:12:34 2002

[illegible]

2 RESULT

31

RESULTS 2 1/C